IN THE SPECIFICATION:

Please replace the paragraph beginning at page 6, line 4, with the following rewritten paragraph:

SubC2>

Q1

—Figure 1 (SEQ ID NO:1) shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a differentially expressed protein provided herein, CHA4. Start (ATG) and stop (TAG) codons are underlined. —

Please replace the paragraph beginning at page 6, line 7, with the following rewritten paragraph:

— Figure 2 (SEQ ID NO:2) shows an embodiment of the amino acid sequence of CHA4.—

Please replace the paragraph beginning at page 7, line 28, with the following rewritten paragraph:

Q2

— In a preferred embodiment, the differentially expressed sequences are those of nucleic acids encoding CHA4 or fragments thereof. Preferably, the differentially expressed sequence is that depicted in figure 1 (SEQ ID NO:1), or a fragment thereof. Preferably, the differentially expressed sequences encode a protein having the amino acid sequence depicted in figure 2 (SEQ ID NO:2), or a fragment thereof. In a preferred embodiment, CHA4 is human Ephrin-A3.—

Please replace the paragraph beginning at page 13, line 8, with the following rewritten paragraph:

Q3

— The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid; SEQ ID NO:3) motif. Immunoglobulin-like domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions.—

Please replace the paragraph beginning at page 15, line 4, with the following rewritten paragraph:

Q4

— In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the figures, preferably those shown in Figures

Q4 cont.

1 and 2 (SEQ ID NOS:1-2) and fragments thereof. In one embodiment the sequences utilized herein are those set forth in the figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the figures. In another embodiment, the sequences are sequence variants as further described herein. –

Please replace the paragraph beginning at page 15, line 31, with the following rewritten paragraph:

Q5

– Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of figure 1 (SEQ ID NO:1). A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.–

Please replace the paragraph beginning at page 46, line 25, with the following rewritten paragraph:

Q6

– In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "differentially expressed proteins" or "cancer modulating proteins". Additionally, "modulator" and "modulating" proteins are sometimes used interchangeably herein. In one embodiment, the differentially expressed protein is termed CHA4. CHA4 sequences can be identified as described herein for differentially expressed sequences. In one embodiment, CHA4 sequences are depicted in Figures 1 and 2 (SEQ ID NOS:1-2). The differentially expressed protein may be a fragment, or alternatively, be the full length protein to the fragment shown herein. Preferably, the differentially expressed protein is a fragment. In a preferred embodiment, the amino acid sequence which is used to determine sequence identity or similarity is that depicted in figure 2. In another embodiment, the sequences are naturally occurring allelic variants of a protein having the sequence depicted in figure 2. In another embodiment, the sequences are sequence variants as further described herein.–